

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 19:58:43 ; Search time 1216.64 Seconds
(without alignments)
12440.963 Million cell updates/sec

Title: US-09-456-306-1

Perfect score: 2160
Sequence: 1 ttgagggcagatctgtgag.....ggtgccatgagatgcct 2160

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
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189: em_estp88:*

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190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	95.8	4.4	538	39	AM036130
C 2	69.8	3.2	467	39	AM036129
3	59.2	2.7	475	16	AI097766
4	59.2	2.7	504	27	AI931656
5	59.2	2.7	827	29	AU079796
6	58	2.7	539	87	AM217660
7	57.6	2.7	845	106	BE282914
8	55.8	2.6	492	4	AA289922
9	55.8	2.6	571	22	AI573836
10	54.2	2.5	451	95	AM763503
11	53.2	2.5	612	39	AM035982
12	51.6	2.4	604	94	AM737588
13	51.6	2.4	636	39	AM031597
14	51.6	2.4	644	39	AM033050
15	51.2	2.4	523	111	BE681144
16	50.8	2.4	482	28	AL383545
17	50.8	2.4	520	93	AM684434
18	50	2.3	560	137	BE924524
19	49.4	2.3	824	134	BE037543
20	48.2	2.2	466	1	AA071233
21	47.8	2.2	357	109	BE521719
22	47.8	2.2	490	105	BE194893
23	47.8	2.2	508	40	AM132431
24	47.2	2.2	565	95	AM776566
25	47	2.2	462	106	BE264847
26	47	2.2	467	106	BE305099
27	47	2.2	497	105	BE249896
28	47	2.2	533	5	AA306411
29	47	2.2	527	106	BE305023
30	47	2.2	585	106	BE305054
31	47	2.2	604	97	AM958734
32	47	2.2	633	108	BE435274
33	47	2.2	771	107	BE408527
34	47	2.2	835	137	BE894277
35	47	2.2	906	105	BE250242
36	47	2.2	948	105	BE250090
37	47	2.2	985	105	BE250061
38	46.6	2.2	510	4	AA254902
39	46.6	2.2	588	87	AM224881
40	46	2.1	466	143	RI17722
41	45.6	2.1	447	12	AA797013
42	45.6	2.1	536	108	BE450711
43	45.6	2.1	561	108	BE449771
44	45.6	2.1	653	24	AT775804
45	45.2	2.1	544	110	BE637311

ALIGNMENTS

```

RESULT 1
AM036130/c
LOCUS
DEFINITION AM036130 538 bp mRNA
ACCESSION EST274506 tomato seed, TMM Lycopersicon esculentum cDNA clone
VERSION CLEFI1 similar to pyruvate oxidase, mRNA sequence.
KEYWORDS AM036130.1 GI:5894809
SOURCE tomato.

```

ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 538)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,M., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
S.D. and Giovannoni,J.
Generation of ESTs from tomato seed tissue
Unpublished (1999)
TITLE JOURNAL
COMMENT Contact: David Fritsch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfritsch@CLEMSON.EDU
5 prime sequence.
FEATURES Location/Qualifiers
source 1..538
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLE1G11"
/clone_1lb="tomato seed, TAMU"
/tissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
BASE COUNT 109 a 154 c 156 g 119 t
ORIGIN
Query Match 4.4%; Score 95.8; DB 39; Length 538;
Best Local Similarity 53.6%; Pred. No. 1.8e-17;
Matches 199; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
QY 465 cgaatgaagaagcggcggttgcagcgggtgcgaatcgtlgtacacttgggagctg 524
11
DB 533 CCCACGATTAAGTGGCGCTTTCGCGCTGAAGCACAACCTTAGCGTAGAAGT 474
413 TGCACACCAATCACCCTTCCGCTACGCGGATTCGCGCTATTTCCCTCCACGAAT 354
QY 525 gcaagatgagcgtctctgtgttcttgcgaacacacactgattcaaggtcttattg 564
11
DB 473 GCGGCTTGGCGGATCGTGGCGCCCGGCAACCTGACTTAATCAACGCGCTTCGAT 414
585 tcgacatgaatgagtgagaggtgtgtgcacatgcagcatatccgagtgccagatt 644
11
DB 413 TGCACACCAATCACCCTTCCGCTACGCGGATTCGCGCTATTTCCCTCCACGAAT 354
QY 645 ggtcgaagcttcttcgaagaacgcacatcgcgagatttgcgttaagaagatgctgttacc 704
11
DB 353 GCGACGCGCTATTTCCAGGAACCCACCAAGAGCTATTCCGCAATGTAAGTACTACTAT 294
QY 705 tgcgagatgtgaatgtgtgtgagcaggttgaaagcatttgcatacgcgattcgctcc 764
11
DB 293 TCGGACTGCTTCCAGCCCGGAGAGATCCCAAGTACTGCGATTGCCATGCCCAAA 234
QY 765 accatggcgggttaagaagtgatgcggtgagtagatccggtgataatcgaagaagac 824
11
DB 233 GCGGCTTCAACCGTGCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT 174
QY 825 gcaagtgacag 835
11 11 11
DB 173 GCGCCAGAGG 163
RESULT 2
AM036129/c AM036129 467 bp mRNA EST 15-SEP-1999

DEFINITION EST274505 tomato seed, TAMU Lycopersicon esculentum cDNA clone
CLE1G23 similar to pyruvate oxidase, mRNA sequence.
ACCESSION AM036129
VERSION AM036129.1 GI:5694808
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 467)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,M., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
S.D. and Giovannoni,J.
Generation of ESTs from tomato seed tissue
Unpublished (1999)
TITLE JOURNAL
COMMENT Contact: David Fritsch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfritsch@CLEMSON.EDU
5 prime sequence.
FEATURES Location/Qualifiers
source 1..467
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLE1G23"
/clone_1lb="tomato seed, TAMU"
/tissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
BASE COUNT 98 a 134 c 132 g 103 t
ORIGIN
Query Match 3.2%; Score 69.8; DB 39; Length 467;
Best Local Similarity 51.8%; Pred. No. 1.1e-09;
Matches 158; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
QY 531 tgtctgctctctgtgtgtctcgaagaacacacactgattcaaggtcttgaatcgcac 590
11
DB 467 TCGCGCGGATCGTGGCGCCCGGCAACCTGACTTAATCAACGCGCTTCGATTCGCAC 408
QY 591 cgaatgagtgagaggtgtgtgcacatgcagcatatccgagtgccagattgttgc 650
11
DB 407 CGCAATCAGGTTCCGCTACGCGGATTCGCGCTATTTCCCTCCAGTGAATTTGCCAGC 348
QY 651 acgtcttcgaagaacgcacatcgcgagatttgcgttaagaagatgctgttaccgag 710
11
DB 347 GCGTATTTCCAGGAACCCACCAAGAGCTATTCCGCAATGTAAGTACTACTACTAT 288
QY 711 atggtgaatgtgtgtgagaggtgaagcatttgcatacgcgattcagttcacacatg 770
11
DB 287 CTGCTTTCAGCCCGGAGAGATCCCAAGTACTGCGGATTCGCAATGCCCAAGCGGTG 228
QY 771 gcgggttaagaagtgatgcggtgagtagtattcctgtgtgataatcgaagaagcaggt 830
11
DB 227 CTAGCGGTGGCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTT 168
QY 831 gacag 835
11 11 11
DB 167 GAAGG 163
RESULT 3

AI097766 475 bp mRNA EST 20-AUG-1998
 LOCUS uc355f02.Y1 Sugano mouse liver mla Mus musculus cDNA clone
 DEFINITION IMAGE:1482363.5' similar to WP.B0334.3A CF02934 ;, mRNA sequence.
 ACCESSION AI097766
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 475)
 AUTHORS
 Marrer,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kneaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Watson,R.
 TITLE The WashU-HIMI Mouse EST Project
 JOURNAL
 COMMENT
 CONTACT: Maria M/Mouse EST Project
 (1996)

FEATURES
source
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:930719
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 264.
Location/Qualifiers
1..475

BASE COUNT	ORIGIN
116 a	107 c
142 g	110 t

	Overy Match	2.7%	Score 59.2;	DB 16,	Length 475;	
	Best Local Similarity	49.7%;	Pred. No.	1.6e-06;		
Mutches	151; Conservative	0;	Mismatches	153;	Indels	Gaps
Oy	361 cttggaagctcaagtgtfagaacgaattatgttggtybgtygaaaccttaaccga					420
Db	162 CTTAAATCTCAAGATTGGAGTACATGTTCCGTTCGTGAAGCATCCCCGCACCATAA					221
Oy	421 tcgtgatgcgtccgccaatcagatatgttgtyggcgacgttcgaaaigaagaacgg					480
Dd	222 TCCTCCTTCTCCCGCACGACTGGSCATCAACATTTGGATGCCGAATGACACAACGG					281
Oy	481 cgagcttgacaaggctcggaatacgttatcacatbtggggagctcgacagtatgtgcgtct					540

Dp	282	CTGTATTAGTGGCCCTCTGCACGTTGGATTATTCGACACAGGAGGCCAGGAGTGTGCTTGTG	341
Oy	541	cttgatggtccctggaacacacacactgattcaaggctcttatgattcgcatacgaatggtg	600
Dp	342	TTTCGTGGTCCCGGTCTGCATCCAGCCCTTGGGGCGCATGGCAATGCAAACTGAACGT	401
Oy	601	cgaaggtcttgccatcgctcgcacatatccgagtcgccgaatggtctgaagttcc	660
Dp	402	GGCCCTTGATTGTGATTGGTGTCTTCTCGAACAATAACGAAGACATGAGGAGCCTTCC	461
Oy	661	agga	664
Dp	462	AGGA	465

RESULT		4
LOCUS	A1931656	
DEFINITION	A1931656 504 bp mRNA EST 30-JUL-1999 U171804.Y1 Sugano mouse kidney mRna Mus musculus cDNA clone IMAGE:136055.5' similar to TR:Q17474 Q17474 B0334.3A.; / RNA sequence.	
ACCESSION	A1931656	
VERSION	A1931656.1	GI:5668141
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS
1 (bases 1 to 504)	Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.

TITLE	JOURNAL	COMMENT
The WashU-NCI Mouse EST Project 1999	Unpublished (1999),	Contact: Marra M/WashU-NCI Mouse EST Project 1999

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1000731

FEATURES	Location/Qualifiers
source	1. .504

```

/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_image="2136055"
/clone_11b="Sugano mouse kidney mklA"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FLJ; Site_1: DraIII
(CACGCTGTG); Site_2: DraII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dt) primer
[ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraII adaptor [TGTGGCCCACTGG], digested
and cloned into distinct draII sites of the pME18S-FLJ
vector (5' site CACGCTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTTAAGAGCTCGc and
primer CGACTTCGACCTTGACACA."
      114 c    150 g    123 t

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/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db.xref="taxon.10090"
/clone_image="3493073"
/clone_id="NCI_CGAP_L129"
/tissue_type="spontaneous tumor, metastatic to mammary.
stem cell origin."
/lab_host="DH10B"
/notes="Organ: Lung; Vector: pcMV-SpOrf6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

```

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:748944"
/clone_1lb="Soares mouse NML"
/tissue_type="Liver"

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FEATURES High quality sequence stop: 1.

Location/Qualifiers
1. .451
source

/organism="Mus musculus"
/strain="129 - C57/B6 - FVB"
/db_xref="taxon:10090"
/clone="IMAGE:3154848"
/clone_1ib="NCI CGAP Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

BASE COUNT 105 a 102 c 128 g 116 t
ORIGIN

Query Match 2.5%; Score 54.2; DB 95; Length 451;
Best Local Similarity 48.5%; Pred. No. 5e-05;

Matches 149; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 358 acacttgaagctcaaggtgaaagcaattatgtgttggtgagacacccataac 417
Db 42 ACGCTCTAAAACCTCAAGATGTGAGTACATGTCGTGTCGTAGCATCCCGGACCG 101

QY 418 cgatctgtagctctgcgcacatcagatattggtggtgacagttcgaataagaag 477
Db 102 AATGCTCTTCTGCTCCAGGACTGGGCAATCAATGATGGGATGGGATGAGCAAT 161

QY 478 cggcgagcttgacagccggtggaatcgttgatcactgaggagagctggcagtatgtgtg 537
Db 162 CGGCTTGTATAGTCCTCTGCACTTGATCCTGACGAGGAGCCAGAGATGTCCCTG 221

QY 538 ctctctgtggtccggaacacacactgattcagggtcttattgatcgcagtaag 597
Db 222 TTGTTTGTGGCCGGCTTATCCACGCGCTGGCGGATGGCAAAATCAATGAAC 281

QY 598 gtgcgaagtggtgacatcgtacatcattccgagagcccaatgtgttcgcgtctc 657
Db 282 GTTGCCCTTATGTGATTTGGTGTGTTCTGTGAGACATATCAAGCTATGGAGCCT 341

QY 658 tccagga 664
Db 342 TCCAGA 348

RESULT 11

AM035982 612 bp mRNA EST 15-SEP-1999
LOCUS

DEFINITION EST282841 tomato callus, TAMU Lycopersicon esculentum cDNA clone
ACCESION AM035982
VERSION AM035982.1 GI:5894738
KEYWORDS EST.

SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 612)
Alcala, V., Vredalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Roming,
C.M., Fraser, C.M., Martin, G.B., Tanksey, S.D. and Giovannoni, J.

TITLE Generation of ESTs from tomato callus tissue
JOURNAL Unpublished (1999)
COMMENT Contact: David Fritsch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

FEATURES
source
1. .612
Location/Qualifiers

Tel: 864 656 4366
Fax: 864 656 4293
Email: dfritsch@CLEMSON.EDU
5 prime sequence.

/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="CLEC3318"
/clone_1ib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"

/lab_host="XLI-Blue MRP"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus Est Library"

BASE COUNT 140 a 157 c 133 g 182 t
ORIGIN

Query Match 2.5%; Score 53.2; DB 39; Length 612;
Best Local Similarity 52.2%; Pred. NO. 0.00011;
Matches 118; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 446 tattgaagtggtgacagttcgaatgagaagcggcggttgacagccggtgcgaatc 505
Db 377 TATTCGTAATGTGCTGTCACAGTCATGAACAGGGGAGTGTTTGCTGCACAGGGTTACGC 436

QY 506 gttatcactgggagagctgagcagtatgctgcttctgtgtcccggaacacacact 565
Db 437 ACGGCTACTGGGTTCCCTGCTGTTGTGATGCTACATCTGCGGAGACTACGAATCA 496

QY 566 gattcaaggtcttatcattcgcacatcgaatggtgagagtggtggcctgctagcca 625
Db 497 TGTTAGCGCTCTTGCATGCTTTGTTGATGATATCCCATGTGTGCTATTAACCGCTCA 556

QY 626 tattcgaagtgccagatggttcgaagcttcttcacgaagacagcat 671
Db 557 AGTCCGAGGAGGATGATTGTACTGATGCGCTTCAAGAAATCTCT 602

RESULT 12

AM737588 604 bp mRNA EST 25-APR-2000
LOCUS

DEFINITION EST339015 tomato flower buds, anthesis, Cornell University
ACCESION AM737588
VERSION AM737588.1 GI:7646533
KEYWORDS EST.

SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 604)
van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang,
F., Hansen, T.S., Craven, M.B., Bowman, C.L., Roming, C.M., Nierman,
W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

TITLE Generation of ESTs from tomato flower tissue, anthesis
JOURNAL Unpublished (1999)
COMMENT Contact: David Fritsch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

FEATURES
source
1. .612
Location/Qualifiers

Tel: 864 656 4366
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Email: dfritsch@CLEMSON.EDU
5 prime sequence.

/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="CLEC3318"
/clone_1ib="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"

/lab_host="XLI-Blue MRP"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus Est Library"

source

1. 604
/organism="Lycopersicon esculentum"
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/clone_1lb="tomato flower buds, anthesis, Cornell University"
/tissue_type="flower"
/dev_stage="anthesis"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT 138 a 154 c 131 g 181 t

ORIGIN

Query Match 2.4%; Score 51.6; DB 94; Length 604;
Best Local Similarity 51.8%; Pred. No. 0.00033;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 446 tatgtggtgggtgacgttcgaatgaggaagcggttcgacgcggtgcggaatc 505
|||||
Db 372 TATTCGTATGTGCTGCCACGTCATGAACAGGGGTGTGTGCTGCACAGGGTTACGC 431
QY 506 gtgatcacctgggagctgagcatatgctgtctctgtgtctgcctggaacacacacct 565
|||||
Db 432 ACCGGCTACTGCGTCCCTGCTGTTTCTATTGCTACATCGCTCCGGAGCTACGAATCT 491
QY 566 gattcagaggtcttattgattcgacatcgaaatggtgcgaagtggtgcacatcgatcga 625
|||||
Db 492 TGTTAGCGGCTTGCATGATGCTTTGATGATGATGATGATGATGATGATGATGATGATG 551
QY 626 tattccgagtgccagatgtgttcgacgttcttcacggaacgcat 671
|||||
Db 552 AGTCCGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597

RESULT 13
AM031597 636 bp mRNA EST 15-SEP-1999
LOCUS EST275051 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC18E17, mRNA sequence.
ACCESSION AM031597
VERSION AM031597.1 GI:5890353
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 636)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue Unpublished (1999)
CONTACT: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prime sequence.
FEATURES
source
1. 636
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC18E17"
/clone_1lb="tomato callus, TAMU"

/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni Laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 153 a 161 c 135 g 187 t

ORIGIN

Query Match 2.4%; Score 51.6; DB 39; Length 636;
Best Local Similarity 51.8%; Pred. No. 0.00034;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 446 tatgtggtgggtgacgttcgaatgaggaagcggttcgacgcggtgcggaatc 505
|||||
Db 374 TATTCGTATGTGCTGCCACGTCATGAACAGGGGTGTGTGCTGCACAGGGTTACGC 433
QY 506 gtgatcacctgggagctgagcatatgctgtctctgtgtctgcctggaacacacacct 565
|||||
Db 434 ACCGGCTACTGCGTCCCTGCTGTTTCTATTGCTACATCGCTCCGGAGCTACGAATCT 493
QY 566 gattcagaggtcttattgattcgacatcgaaatggtgcgaagtggtgcacatcgatcga 625
|||||
Db 494 TGTTAGCGGCTTGCATGATGCTTTGATGATGATGATGATGATGATGATGATGATGATG 553
QY 626 tattccgagtgccagatgtgttcgacgttcttcacggaacgcat 671
|||||
Db 554 AGTCCGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599

RESULT 14
AM033050 644 bp mRNA EST 15-SEP-1999
LOCUS EST276609 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC21L2, mRNA sequence.
ACCESSION AM033050
VERSION AM033050.1 GI:5891806
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 644)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue Unpublished (1999)
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Clemson University Genomics Institute
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Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prime sequence.
FEATURES
source
1. 644
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC21L2"
/clone_1lb="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni Laboratory; cLEC - Cotyledons

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/db_xref="taxon:835"
/clone="XENOPUS_SOURCE_ID:xlinga002n24"
/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"

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